

OIEP

RAW SEQUENCE LISTING

DATE: 04/27/2001

PATENT APPLICATION: US/09/832,929

TIME: 13:13:08

Input Set : A:\PF547SL.txt

Output Set: N:\CRF3\04272001\I832929.raw

3 <110> APPLICANT: Rosen, Craig A.
 4 Haseltine, William A.
 6 <120> TITLE OF INVENTION: Albumin Fusion Proteins
 8 <130> FILE REFERENCE: PF547
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/832,929
 11 <141> CURRENT FILING DATE: 2001-04-12
 13 <150> PRIOR APPLICATION NUMBER: 60/229,358
 14 <151> PRIOR FILING DATE: 2000-04-12
 16 <150> PRIOR APPLICATION NUMBER: 60/256,931
 17 <151> PRIOR FILING DATE: 2000-12-21
 19 <150> PRIOR APPLICATION NUMBER: 60/199,384
 20 <151> PRIOR FILING DATE: 2000-04-25
 22 <160> NUMBER OF SEQ ID NOS: 72
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 23
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <221> NAME/KEY: primer_bind
 33 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 35 <400> SEQUENCE: 1
 36 cccaagaatt cccttatcca ggc 23
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 33
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Artificial Sequence
 44 <220> FEATURE:
 45 <221> NAME/KEY: primer_bind
 46 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 48 <400> SEQUENCE: 2
 49 gggagctta gaagccacag gatccctcca cag 33
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 16
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <221> NAME/KEY: misc_structure
 59 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 60 with non-cohesive ends.
 62 <400> SEQUENCE: 3
 63 gataaagatt cccaac 16
 66 <210> SEQ ID NO: 4
 67 <211> LENGTH: 17
 68 <212> TYPE: DNA
 69 <213> ORGANISM: Artificial Sequence
 71 <220> FEATURE:

ENTERED

sec p. 5

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72 <221> NAME/KEY: misc_structure
73 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
74     with non-cohesive ends.
76 <400> SEQUENCE: 4
77 aattgttggg aatcttt                                     17
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 17
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <221> NAME/KEY: misc_structure
87 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
88     with non-cohesive ends.
90 <400> SEQUENCE: 5
91 ttaggcttat tccaac                                     17
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 18
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <221> NAME/KEY: misc_structure
101 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
102     with non-cohesive ends.
104 <400> SEQUENCE: 6
105 aattgttggg aataagcc                                     18
108 <210> SEQ ID NO: 7
109 <211> LENGTH: 24
110 <212> TYPE: PRT
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <221> NAME/KEY: SITE
115 <222> LOCATION: 1)..(19)
116 <223> OTHER INFORMATION: invertase leader sequence
118 <220> FEATURE:
119 <221> NAME/KEY: SITE
120 <222> LOCATION: 20)..(24)
121 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
123 <400> SEQUENCE: 7
124 Met Leu Leu Gln Ala Phe Leu Phe Leu Ala Gly Phe Ala Ala Lys
125   1      5      10      15
127 Ile Ser Ala Asp Ala His Lys Ser
128           20
131 <210> SEQ ID NO: 8
132 <211> LENGTH: 21
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <221> NAME/KEY: misc_structure
138 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA

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139      fragments with non-cohesive ends.
141 <400> SEQUENCE: 8
142 gagatgcaca cctgagtga g                               21
145 <210> SEQ ID NO: 9
146 <211> LENGTH: 27
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <221> NAME/KEY: misc_structure
152 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
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155 <400> SEQUENCE: 9
156 gatcctgtgg cttcgatgca cacaaga                       27
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 24
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <221> NAME/KEY: misc_structure
166 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
167      fragments with non-cohesive ends.
169 <400> SEQUENCE: 10
170 ctcttggtgtg catcgaagcc acag                          24
173 <210> SEQ ID NO: 11
174 <211> LENGTH: 30
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <221> NAME/KEY: misc_structure
180 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
181      fragments with non-cohesive ends.
183 <400> SEQUENCE: 11
184 tgtggaagag cctcagaatt tattcccaac                     30
187 <210> SEQ ID NO: 12
188 <211> LENGTH: 31
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <221> NAME/KEY: misc_structure
194 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
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197 <400> SEQUENCE: 12
198 aattgttggg aataaattct gaggtctttc c                   31
201 <210> SEQ ID NO: 13
202 <211> LENGTH: 47
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <221> NAME/KEY: misc_structure

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208 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
209     fragments with non-cohesive ends.
211 <400> SEQUENCE: 13
212 ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac      47
215 <210> SEQ ID NO: 14
216 <211> LENGTH: 48
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <221> NAME/KEY: misc_structure
222 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
223     fragments with non-cohesive ends.
225 <400> SEQUENCE: 14
226 aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc      48
229 <210> SEQ ID NO: 15
230 <211> LENGTH: 62
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <221> NAME/KEY: misc_structure
236 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
237     fragments with non-cohesive ends.
239 <400> SEQUENCE: 15
240 ttaggcttag gcggtggtgg atctggtggc ggcgatctg gtggcggtgg atccttccca 60
241 ac      62
244 <210> SEQ ID NO: 16
245 <211> LENGTH: 63
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <221> NAME/KEY: misc_structure
251 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
252     fragments with non-cohesive ends.
254 <400> SEQUENCE: 16
255 aattgttggg aagatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60
256 gcc      63
259 <210> SEQ ID NO: 17
260 <211> LENGTH: 1782
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
265 <221> NAME/KEY: CDS
266 <222> LOCATION: (1)..(1755)
269 <400> SEQUENCE: 17
270 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa      48
271 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
272   1           5           10           15
274 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag      96
275 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

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276	20	25	30	
278	cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa	144		
279	Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu			
280	35 40 45			
282	ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa	192		
283	Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys			
284	50 55 60			
286	tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt	240		
287	Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu			
288	65 70 75 80			
290	cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct	288		
291	Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro			
292	85 90 95			
294	gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc	336		
295	Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu			
296	100 105 110			
298	ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat	384		
299	Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His			
300	115 120 125			
302	gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga	432		
303	Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg			
304	130 135 140			
306	aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480		
307	Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
308	145 150 155 160			
310	tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528		
311	Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
312	165 170 175			
314	tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576		
315	Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
316	180 185 190			
318	tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624		
319	Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
320	195 200 205			
322	aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672		
323	Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
324	210 215 220			
326	aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720		
327	Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
328	225 230 235 240			
330	gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768		
331	Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
332	245 250 255			
334	agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816		
335	Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
336	260 265 270			
338	agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864		
339	Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
340	275 280 285			

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/832,929

DATE: 04/27/2001

TIME: 13:13:09

Input Set : A:\PF547SL.txt

Output Set: N:\CRF3\04272001\I832929.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:639 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:644 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:654 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:659 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:664 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:674 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:679 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:684 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:689 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:694 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:699 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:704 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25

L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25

L:723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:738 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:748 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

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L:763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:768 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:773 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:778 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:783 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26

L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26

L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:817 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:822 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:832 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:837 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:842 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

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L:852 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:857 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:862 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:872 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:877 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

L:882 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27

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L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:902 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:907 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:912 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:917 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:922 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33